

## EXHIBIT F

ClustalW (v1.4) multiple sequence alignment

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huLGR8-C      1 MIVFLVFKHLFSLRLITMFFLLHFIVLINVKDFALTQGSMITPSCQKGYF  50
huLGR8-C_N    1                                     QGSMITPSCQKGYF  14
                                     *****

huLGR8-C      51 PCGNLTKCLPRAFHCDGKDDCGNGADEENCGDTSGWATIFGTVHGNANSV 100
huLGR8-C_N    15 PCGNLTKCLPRAFHCDGKDDCGNGADEENCGDTSGWATIFGTVHGNANSV  64
               *****

huLGR8-C      101 ALTQECFLKQYPQCCDCKETELCVNGDLKSVP MISNNVTLLSLKKNKIH 150
huLGR8-C_N    65 ALTQECFLKQYPQCCDCKETELCVNGDLKSVP MISNNVTLLSLKKNKIH 114
               *****

huLGR8-C      151 SLPDKVFIKYTKLKKIFLQHNCIRHISRKAFFGLCNLQILILDDNPITRI 200
huLGR8-C_N    115 SLPDKVFIKYTKLKKIFLQHNCIRHISRKAFFGLCNLQILILDDNPITRI 164
               *****

huLGR8-C      201 SQRLFTGLNSLFFLSMVNNYLEALPKQMCAQMPQLNWVDLEGNRIKYL TN 250
huLGR8-C_N    165 SQRLFTGLNSLFFLSMVNNYLEALPKQMCAQMPQLNWVDLEGNRIKYL TN 214
               *****

huLGR8-C      251 STFLSCDSLTVLDLSSNTITELSPHLFKDLKLLQKLDLERIEIPNINTRM 300
huLGR8-C_N    215 STFLSCDSLTVLDLSSNTITELSPHLFKDLKLLQKLDLERIEIPNINTRM 264
               *****

huLGR8-C      301 FQPMKNLSHIYFKNFRYCSYAPHVRCMPLTDGISSFEDLLANNILRIFV 350
huLGR8-C_N    265 FQPMKNLSHIYFKNFRYCSYAPHVRCMPLTDGISSFEDLLANNILR  311
               *****

huLGR8-C      351 WVIAFITCFGNLFVIGMRSFIKAENTTHAMSIKILCCADCLMGVYLFFVG 400
huLGR8-C_N    312                                     311

huLGR8-C      401 IFDIKYRGQYQKYALLWMESVQCRLMGFLAMLSTEVSVLLLTLYLTLEKFL 450
huLGR8-C_N    312                                     311

huLGR8-C      451 VIVFPFSNIRPGKRQTSVILICIWMAGFLIAVIPFWNKDYFGNFYKNGV 500
huLGR8-C_N    312                                     311

huLGR8-C      501 CFPLYDQTEDIGSKGYSLGIFLGVNLLAFLIIVFSYITMFCSIQKTALQ 550
huLGR8-C_N    312                                     311

huLGR8-C      551 TTEVRNCFGREVAVANRFFFIVFSDAICWIPVFVVKILSLFRVEIPDTMT 600
huLGR8-C_N    312                                     311

huLGR8-C      601 SWIVIFFLPVNSALNPILYTLTTNFFKDKLKQLLHKHQKRSIFKIKKKSL 650
huLGR8-C_N    312                                     311

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huLGR8-C 651 STSIVWIEDSSSLKLGVLNKITLGDSIMKPVS 682  
huLGR8-C\_N 312 311